

DAVI186.004APC_SEQLIST.TXT

SEQUENCE LISTING

<110> Olayioye, Monilola
 Visvader, Jane
 Lindeman, Geoffrey
 Hoffmann, Peter
 Pomorski, Thomas

<120> A NOVEL PHOSPHOPROTEIN

<130> DAVI186.004APC

<140> 10/538,704

<141> 2005-06-10

<150> PCT/AU03/01664

<151> 2003-12-12

<150> AU 2002953341

<151> 2002-12-13

<160> 7

<170> FastSEQ for windows version 4.0

<210> 1

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<212> PRT

<213> Artificial Sequence

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<223> peptide

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 1 5 10 15
 Ser Arg

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DAVI186.004APC_SEQLIST.TXT

<400> 3

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 1 5 10 15
 Ser Arg

<210> 4

<211> 876

<212> DNA

<213> Homo sapiens

<400> 4

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gtgggctgga	acctgacctg	tagcagggct	gggggtgtctg	tctgggtgca	ggctgtggag	180
atggatcgga	cgctgcacaa	gatcaagtgc	cggatggagt	gctgtgatgt	gccagccgag	240
acactctacg	acgtcctaca	cgacattgag	taccgcaaga	aatgggacag	caacgtcatt	300
gagacttttg	acatcgcccc	cttgacagtc	aacgctgacg	tgggctatta	ctcctggagg	360
tgtcccaagc	ccctgaagaa	ccgtgatgtc	atcaccttcc	gctcctggct	ccccatgggc	420
gctgattaca	tcattatgaa	ctactcagtc	aaacatccca	aatacccacc	tcggaaaagac	480
ttggtccgag	ctgtgtccat	ccagacgggc	tacctcatcc	agagcacagg	gcccgaagagc	540
tgcgtcatca	cctacctggc	ccaggtggac	cccaaaggct	ccttacccaa	gtgggtgggtg	600
aataaatctt	ctcagttcct	ggctcccaag	gccatgaaga	agatgtacaa	ggcgtgcctc	660
aagtaccccg	agtggaaaca	gaagcacctg	cctcacttca	agccgtggct	gcacccggag	720
cagagcccgt	tgccgagcct	ggcgtgtcgc	gagctgtcgg	tgacagcatgc	ggactcactg	780
gagaacatcg	acgagagcgc	ggcggccgag	agcagagagg	agcggatggg	cggcgcgggc	840
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<212> PRT

<213> Homo sapiens

<400> 5

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		20					25					30			
Phe	Arg	Ser	Glu	Cys	Glu	Ala	Glu	Val	Gly	Trp	Asn	Leu	Thr	Tyr	Ser
		35					40					45			
Arg	Ala	Gly	Val	Ser	Val	Trp	Val	Gln	Ala	Val	Glu	Met	Asp	Arg	Thr
		50					55				60				
Leu	His	Lys	Ile	Lys	Cys	Arg	Met	Glu	Cys	Cys	Asp	Val	Pro	Ala	Glu
65					70					75					80
Thr	Leu	Tyr	Asp	Val	Leu	His	Asp	Ile	Glu	Tyr	Arg	Lys	Lys	Trp	Asp
			85						90					95	
Ser	Asn	Val	Ile	Glu	Thr	Phe	Asp	Ile	Ala	Arg	Leu	Thr	Val	Asn	Ala
			100						105					110	
Asp	Val	Gly	Tyr	Tyr	Ser	Trp	Arg	Cys	Pro	Lys	Pro	Leu	Lys	Asn	Arg
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Asp	Val	Ile	Thr	Leu	Arg	Ser	Trp	Leu	Pro	Met	Gly	Ala	Asp	Tyr	Ile
		130				135					140				
Ile	Met	Asn	Tyr	Ser	Val	Lys	His	Pro	Lys	Tyr	Pro	Pro	Arg	Lys	Asp
145					150					155					160
Leu	Val	Arg	Ala	Val	Ser	Ile	Gln	Thr	Gly	Tyr	Leu	Ile	Gln	Ser	Thr
			165						170					175	
Gly	Pro	Lys	Ser	Cys	Val	Ile	Thr	Tyr	Leu	Ala	Gln	Val	Asp	Pro	Lys
			180					185					190		
Gly	Ser	Leu	Pro	Lys	Trp	Val	Val	Asn	Lys	Ser	Ser	Gln	Phe	Leu	Ala
		195				200						205			
Pro	Lys	Ala	Met	Lys	Lys	Met	Tyr	Lys	Ala	Cys	Leu	Lys	Tyr	Pro	Glu
210						215					220				

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Trp Lys Gln Lys His Leu Pro His Phe Lys Pro Trp Leu His Pro Glu
 225 230 235 240
 Gln Ser Pro Leu Pro Ser Leu Ala Leu Ser Glu Leu Ser Val Gln His
 245 250 255
 Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val Ala Glu Ser Arg
 260 265 270
 Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser Asp Asp Asp Thr
 275 280 285
 Ser Leu Thr
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<210> 6
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 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Gln Glu Gly Gly Val Thr Ser Ala Ala Ser Thr Leu Ser Glu Pro
 35 40 45
 Pro Arg Arg Thr Gln Glu Ser Arg Thr Arg Thr Arg Ala Leu Gly Leu
 50 55 60
 Pro Thr Leu Pro Met Glu Lys Leu Ala Ala Ser Thr Glu Pro Gln Gly
 65 70 75 80
 Pro Arg Pro Val Leu Gly Arg Glu Ser Val Gln Val Pro Asp Asp Gln
 85 90 95
 Asp Phe Arg Ser Phe Arg Ser Glu Cys Glu Ala Glu Val Gly Trp Asn
 100 105 110
 Leu Thr Tyr Ser Arg Ala Gly Val Ser Val Trp Val Gln Ala Val Glu
 115 120 125
 Met Asp Arg Thr Leu His Lys Ile Lys Cys Arg Met Glu Cys Cys Asp
 130 135 140
 Val Pro Ala Glu Thr Leu Tyr Asp Val Leu His Asp Ile Glu Tyr Arg
 145 150 155 160
 Lys Lys Trp Asp Ser Asn Val Ile Glu Thr Phe Asp Ile Ala Arg Leu
 165 170 175
 Thr Val Asn Ala Asp Val Gly Tyr Tyr Ser Trp Arg Cys Pro Lys Pro
 180 185 190
 Leu Lys Asn Arg Asp Val Ile Thr Leu Arg Ser Trp Leu Pro Met Gly
 195 200 205
 Ala Asp Tyr Ile Ile Met Asn Tyr Ser Val Lys His Pro Lys Tyr Pro
 210 215 220
 Pro Arg Lys Asp Leu Val Arg Ala Val Ser Ile Gln Thr Gly Tyr Leu
 225 230 235 240
 Ile Gln Ser Thr Gly Pro Lys Ser Cys Val Ile Thr Tyr Leu Ala Gln
 245 250 255
 Val Asp Pro Lys Gly Ser Leu Pro Lys Trp Val Val Asn Lys Ser Ser
 260 265 270
 Gln Phe Leu Ala Pro Lys Ala Met Lys Lys Met Tyr Lys Ala Cys Leu
 275 280 285
 Lys Tyr Pro Glu Trp Lys Gln Lys His Leu Pro His Phe Lys Pro Trp
 290 295 300
 Leu His Pro Glu Gln Ser Pro Leu Pro Ser Leu Ala Leu Ser Glu Leu
 305 310 315 320
 Ser Val Gln His Ala Asp Ser Leu Glu Asn Ile Asp Glu Ser Ala Val
 325 330 335
 Ala Glu Ser Arg Glu Glu Arg Met Gly Gly Ala Gly Gly Glu Gly Ser
 340 345 350
 Asp Asp Asp Thr Ser Leu Thr

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<210> 7
 <211> 214
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 35 40 45
 Thr Gly Leu His Glu Tyr Lys Val Phe Gly Val Leu Glu Asp Cys Ser
 50 55 60
 Pro Thr Leu Leu Ala Asp Ile Tyr Met Asp Ser Asp Tyr Arg Lys Gln
 65 70 75 80
 Trp Asp Gln Tyr Val Lys Glu Leu Tyr Glu Gln Glu Cys Asn Gly Glu
 85 90 95
 Thr Val Val Tyr Trp Glu Val Lys Tyr Pro Phe Pro Met Ser Asn Arg
 100 105 110
 Asp Tyr Val Tyr Leu Arg Gln Arg Arg Asp Leu Asp Met Glu Gly Arg
 115 120 125
 Lys Ile His Val Ile Leu Ala Arg Ser Thr Ser Met Pro Gln Leu Gly
 130 135 140
 Glu Arg Ser Gly Val Ile Arg Val Lys Gln Tyr Lys Gln Ser Leu Ala
 145 150 155 160
 Ile Glu Ser Asp Gly Lys Lys Gly Ser Lys Val Phe Met Tyr Tyr Phe
 165 170 175
 Asp Asn Pro Gly Gly Gln Ile Pro Ser Trp Leu Ile Asn Trp Ala Ala
 180 185 190
 Lys Asn Gly Val Pro Asn Phe Leu Lys Asp Met Ala Arg Ala Cys Gln
 195 200 205
 Asn Tyr Leu Lys Lys Thr
 210